

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: CIBA-GEIGY AG
- (B) STREET: Klybeckstr. 141
- (C) CITY: Basel
- (E) COUNTRY: SCHWEIZ
- (F) POSTAL CODE (ZIP): 4002
- (G) TELEPHONE: +41 61 69 11 11
- (H) TELEFAX: + 41 61 696 79 76
- (I) TELEX: 962 991

(ii) TITLE OF INVENTION: Bifunctional Protein, Preparation and Use

(iii) NUMBER OF SEQUENCES: 11

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..728
- (D) OTHER INFORMATION: /product= "scFv(FRP)5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCTTCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA CTG AAG AAG CCT
Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro
1 5 10

006590"479660

GGA Gly 15	GAG Glu	ACA Thr	GTC Val	AAG Lys	ATC Ile 20	TCC Ser	TGC Cys	AAG Lys	GCC Ala	TCT Ser 25	GGG Gly	TAT Tyr	CCT Pro	TTC Phe	ACA Thr 30	98
AAC Asn	TAT Tyr	GGA Gly	ATG Met	AAC Asn 35	TGG Trp	GTG Val	AAG Lys	CAG Gln	GCT Ala 40	CCA Pro	GGA Gly	CAG Gln	GGT Gly	TTA Leu 45	AAG Lys	146
TGG Trp	ATG Met	GGC Gly	TGG Trp 50	ATT Ile	AAC Asn	ACT Thr	TCC Ser	ACT Thr 55	GGA Gly	GAG Glu	TCA Ser	ACA Thr	TTT Phe 60	GCT Ala	GAT Asp	194
GAC Asp	TTC Phe	AAG Lys 65	GGA Gly	CGG Arg	TTT Phe	GAC Asp	TTC Phe 70	TCT Ser	TTG Leu	GAA Glu	ACC Thr	TCT Ser 75	GCC Ala	AAC Asn	ACT Thr	242
GCC Ala	TAT Tyr 80	TTG Leu	CAG Gln	ATC Ile	AAC Asn	AAC Asn 85	CTC Leu	AAA Lys	AGT Ser	GAA Glu	GAC Asp 90	ATG Met	GCT Ala	ACA Thr	TAT Tyr	290
TTC Phe 95	TGT Cys	GCA Ala	AGA Arg	TGG Trp	GAG Glu 100	GTT Val	TAC Tyr	CAC His	GGC Gly	TAC Tyr 105	GTT Val	CCT Pro	TAC Tyr	TGG Trp 110	GGC Gly	338
CAA Gln	GGG Gly	ACC Thr	ACG Thr 115	GTC Val	ACC Thr	GTT Val	TCC Ser	TCT Ser	GGC Gly 120	GGT Gly	GGC Gly	GGT Gly	TCT Ser 125	GGT Gly	GGC Gly	386
GGT Gly	GGC Gly	TCC Ser	GGC Gly 130	GGT Gly	GGC Gly	GGT Gly	TCT Ser	GAC Asp 135	ATC Ile	CAG Gln	CTG Leu	ACC Thr	CAG Gln 140	TCT Ser	CAC His	434
AAA Lys	TTC Phe	CTG Leu 145	TCC Ser	ACT Thr	TCA Ser	GTA Val	GGA Gly 150	GAC Asp	AGG Arg	GTC Val	AGC Ser	ATC Ile 155	ACC Thr	TGC Cys	AAG Lys	482
GCC Ala 160	AGT Ser	CAG Gln	GAT Asp	GTG Val	TAT Tyr	AAT Asn 165	GCT Ala	GTT Val	GCC Ala	TGG Trp	TAT Tyr 170	CAA Gln	CAG Gln	AAA Lys	CCA Pro	530
GGA Gly 175	CAA Gln	TCT Ser	CCT Pro	AAA Lys	CTT Leu 180	CTG Leu	ATT Ile	TAC Tyr	TCG Ser	GCA Ala 185	TCC Ser	TCC Ser	CGG Arg	TAC Tyr	ACT Thr 190	578
GGA Gly	GTC Val	CCT Pro	TCT Ser	CGC Arg 195	TTC Phe	ACT Thr	GGC Gly	AGT Ser	GGC Gly 200	TCT Ser	GGG Gly	CCG Pro	GAT Asp	TTC Phe 205	ACT Thr	626
TTC Phe	ACC Thr	ATC Ile	AGC Ser 210	AGT Ser	GTG Val	CAG Gln	GCT Ala	GAA Glu 215	GAC Asp	CTG Leu	GCA Ala	GTT Val	TAT Tyr 220	TTC Phe	TGT Cys	674

CAG CAA CAT TTT CGT ACT CCA TTC ACG TTC GGC TCG GGG ACA AAA TTG 722
Gln Gln His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu
225 230 235

GAG ATC TAGCTGATCA AAGCTCTAGA 748
Glu Ile
240

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr
20 25 30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
35 40 45
Gly Trp Ile Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe
50 55 60
Lys Gly Arg Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
65 70 75 80
Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys
85 90 95
Ala Arg Trp Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly
100 105 110
Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125
Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe
130 135 140
Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
145 150 155 160
Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
165 170 175

006T90"47296560

Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val
180 185 190
Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr
195 200 205
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220
His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
225 230 235 240

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 748 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..728
- (D) OTHER INFORMATION: /product= "scFv (FWP51)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AAGCTTCT CAG GTA CAA CTG CAG CAG TCT GGG GCT GAG CTG GTG AGG CCT 50
Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro
1 5 10
GGG ACT TCA GTG AAG CTG TCC TGC AAG GCT TCT GAT TAC ACC TTC ACC 98
Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Asp Tyr Thr Phe Thr
15 20 25 30
AGC TAC TGG ATG AAC TGG GTG AAG CAG AGG CCT GGA CAA GGC CTT GAA 146
Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu
35 40 45
TGG ATT GGT ATG ATT GAT CCT TCA GAC AGT GAA ACT CAA TAC AAT CAA 194
Trp Ile Gly Met Ile Asp Pro Ser Asp Ser Glu Thr Gln Tyr Asn Gln
50 55 60
ATG TTC AAG GAC AAG GCC GCA TTG ACT GTA GAC AAG TCC TCC AAT ACA 242
Met Phe Lys Asp Lys Ala Ala Leu Thr Val Asp Lys Ser Ser Asn Thr
65 70 75

006T90"4296660

0059674-061900

GCC TAC ATG CAA CTC AGC AGC CTG ACA TCT GAG GAC TCT GCG GTC TAT Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr 80 85 90	290
TAC TGT GCA AAA GGG GGG GCC TCT GGG GAC TGG TAC TTC GAT GTC TGG Tyr Cys Ala Lys Gly Gly Ala Ser Gly Asp Trp Tyr Phe Asp Val Trp 95 100 105 110	338
GGC CAA GGG ACC ACG GTC ACC GTT TCC TCT GGC GGT GGC GGT TCT GGT Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly 115 120 125	386
GGC GGT GGC TCC GGC GGT GGC GGT TCT GAC ATC CAG CTG ACC CAG TCT Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser 130 135 140	434
CCA TCC TCA CTG TCT GCA TCT CTG GGA GGC GAA GTC ACC ATC ACT TGC Pro Ser Ser Leu Ser Ala Ser Leu Gly Gly Glu Val Thr Ile Thr Cys 145 150 155	482
AAG GCA AGC CAA GAC ATT AAG AAG TAT ATA GCT TGG TAC CAA CAC AAG Lys Ala Ser Gln Asp Ile Lys Lys Tyr Ile Ala Trp Tyr Gln His Lys 160 165 170	530
CCT GGA AAA AGT CCT CGG CTA CTC ATA CAC TAC ACA TCT GTA TTA CAG Pro Gly Lys Ser Pro Arg Leu Leu Ile His Tyr Thr Ser Val Leu Gln 175 180 185 190	578
CCA GGC ATC CCA TCC AGG TTC AGT GGA AGT GGG TCT GGG AGA GAT TAT Pro Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr 195 200 205	626
TCC TTC AGC ATC CAC AAC CTG GAG CCT GAA GAT ATT GCA ACT TAT TAT Ser Phe Ser Ile His Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr 210 215 220	674
TGT CTA CAT TAT GAT TAT CTG TAC ACG TTC GGA GGG GGC ACC AAG CTG Cys Leu His Tyr Asp Tyr Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu 225 230 235	722
GAG ATC TAGCTGATCA AAGCTCTAGA Glu Ile 240	748

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Thr
1 5 10 15
Ser Val Lys Leu Ser Cys Lys Ala Ser Asp Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Met Ile Asp Pro Ser Asp Ser Glu Thr Gln Tyr Asn Gln Met Phe
50 55 60
Lys Asp Lys Ala Ala Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Gly Gly Ala Ser Gly Asp Trp Tyr Phe Asp Val Trp Gly Gln
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
130 135 140
Ser Leu Ser Ala Ser Leu Gly Gly Glu Val Thr Ile Thr Cys Lys Ala
145 150 155 160
Ser Gln Asp Ile Lys Lys Tyr Ile Ala Trp Tyr Gln His Lys Pro Gly
165 170 175
Lys Ser Pro Arg Leu Leu Ile His Tyr Thr Ser Val Leu Gln Pro Gly
180 185 190
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Arg Asp Tyr Ser Phe
195 200 205
Ser Ile His Asn Leu Glu Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Leu
210 215 220
His Tyr Asp Tyr Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1479 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 40..1422
(D) OTHER INFORMATION: /product= "leader-scFv(FRP5):lyt-2
hinge:zeta"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

006T90"4296550

GAATTCGGCA CGAGCTTAAG GCACCACTTC TTAGACATC	ATG GCT TGG GTG TGG	54
	Met Ala Trp Val Trp	
	1 5	
ACC TTG CTA TTC CTG ATG GCA GCT GCC AAA GTG CCC AAG CAG ATC CAG		102
Thr Leu Leu Phe Leu Met Ala Ala Ala Lys Val Pro Lys Gln Ile Gln		
	10 15 20	
TTG GTG CAG TCT GGA CCT GAG CTG AAG AAG CCT GGA GAG ACA GTC AAG		150
Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys		
	25 30 35	
ATC TCC TGC AAG GCC TCT GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC		198
Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn		
	40 45 50	
TGG GTG AAG CAG GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT		246
Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile		
	55 60 65	
AAC ACC TCC ACT GGA GAG TCA ACA TTT GCT GAT GAC TTC AAG GGA CGG		294
Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg		
	70 75 80 85	
TTT GAC TTC TCT TTG GAA ACC TCT GCC AAC ACT GCC TAT TTG CAG ATC		342
Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile		
	90 95 100	
AAC AAC CTC AAA AGT GAA GAC ATG GCT ACA TAT TTC TGT GCA AGA TGG		390
Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp		
	105 110 115	
GAG GTT TAC CAC GGC TAC GTT CCT TAC TGG GGC CAA GGG ACC ACG GTC		438
Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val		
	120 125 130	

ACC	GTT	TCC	TCT	GGC	GGT	GGC	GGT	TCT	GGT	GGC	GGT	GGC	TCC	GGC	GGT	486
Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
	135						140					145				
GGC	GGT	TCT	GAC	ATC	CAG	CTG	ACC	CAG	TCT	CAC	AAA	TTC	CTG	TCC	ACT	534
Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	His	Lys	Phe	Leu	Ser	Thr	
	150				155					160					165	
TCA	GTA	GGA	GAC	AGG	GTC	AGC	ATC	ACC	TGC	AAG	GCC	AGT	CAG	GAT	GTG	582
Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	
				170					175					180		
TAT	AAT	GCT	GTT	GCC	TGG	TAT	CAA	CAG	AAA	CCA	GGA	CAA	TCT	CCT	AAA	630
Tyr	Asn	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	
			185					190					195			
CTT	CTG	ATT	TAC	TCG	GCA	TCC	TCC	CGG	TAC	ACT	GGA	GTC	CCT	TCT	CGC	678
Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Tyr	Thr	Gly	Val	Pro	Ser	Arg	
		200					205					210				
TTC	ACT	GGC	AGT	GGC	TCT	GGG	CCG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	AGT	726
Phe	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
	215					220					225					
GTG	CAG	GCT	GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAA	CAT	TTT	CGT	774
Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	His	Phe	Arg	
	230				235					240					245	
ACT	CCA	TTC	ACG	TTC	GGC	TCG	GGG	ACA	AAA	TTG	GAG	ATC	AAA	GCT	CTA	822
Thr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ala	Leu	
				250				255					260			
GAG	ATC	AGC	AAC	TCG	GTG	ATG	TAC	TTC	AGT	TCT	GTC	GTG	CCA	GTC	CTT	870
Glu	Ile	Ser	Asn	Ser	Val	Met	Tyr	Phe	Ser	Ser	Val	Val	Pro	Val	Leu	
			265					270					275			
CAG	AAA	GTG	AAC	TCT	ACT	ACT	ACC	AAG	CCA	GTG	CTG	CGA	ACT	CCC	TCA	918
Gln	Lys	Val	Asn	Ser	Thr	Thr	Thr	Lys	Pro	Val	Leu	Arg	Thr	Pro	Ser	
	280						285					290				
CCT	GTG	CAC	CCT	ACC	GGG	ACA	TCT	CAG	CCC	CAG	AGA	CCA	GAA	GAT	TGT	966
Pro	Val	His	Pro	Thr	Gly	Thr	Ser	Gln	Pro	Gln	Arg	Pro	Glu	Asp	Cys	
	295					300					305					
CGG	CCC	CGT	GGC	TCA	GTG	AAG	GGG	ACC	GGA	TTG	GAC	TTT	CTA	GAG	GAT	1014
Arg	Pro	Arg	Gly	Ser	Val	Lys	Gly	Thr	Gly	Leu	Asp	Phe	Leu	Glu	Asp	
	310				315					320					325	
CCC	AAA	CTC	TGC	TAC	TTG	CTA	GAT	GGA	ATC	CTC	TTC	ATC	TAC	GGA	GTC	1062
Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu	Phe	Ile	Tyr	Gly	Val	
				330					335					340		

006790"4.061900

ATC ATC ACA GCC CTG TAC CTG AGA GCA AAA TTC AGC AGG AGT GCA GAG 1110
 Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu
 345 350 355

ACT GCT GCC AAC CTG CAG GAC CCC AAC CAG CTC TAC AAT GAG CTC AAT 1158
 Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn
 360 365 370

CTA GGG CGA AGA GAG GAA TAT GAC GTC TTG GAG AAG AAG CGG GCT CGG 1206
 Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg
 375 380 385

GAT CCA GAG ATG GGA GGC AAA CAG CAG AGG AGG AGG AAC CCC CAG GAA 1254
 Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu
 390 395 400 405

GGC GTA TAC AAT GCA CTG CAG AAA GAC AAG ATG GCA GAA GCC TAC AGT 1302
 Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
 410 415 420

GAG ATC GGC ACA AAA GGC GAG AGG CGG AGA GGC AAG GGG CAC GAT GGC 1350
 Glu Ile Gly Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
 425 430 435

CTT TAC CAG GGT CTC AGC ACT GCC ACC AAG GAC ACC TAT GAT GCC CTG 1398
 Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
 440 445 450

CAT ATG CAG ACC CTG GCC CCT CGC TAACAGCCAG GGCATTTCTC CCTCACGGGC 1452
 His Met Gln Thr Leu Ala Pro Arg
 455 460

AGATCCCCGG GTACCGAGCT CGAATTC 1479

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Lys Val
 1 5 10 15

Pro Lys Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
 20 25 30

Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr
 35 40 45

Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys
50						55					60				
Trp	Met	Gly	Trp	Ile	Asn	Thr	Ser	Thr	Gly	Glu	Ser	Thr	Phe	Ala	Asp
65					70					75					80
Asp	Phe	Lys	Gly	Arg	Phe	Asp	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Asn	Thr
				85					90					95	
Ala	Tyr	Leu	Gln	Ile	Asn	Asn	Leu	Lys	Ser	Glu	Asp	Met	Ala	Thr	Tyr
			100					105					110		
Phe	Cys	Ala	Arg	Trp	Glu	Val	Tyr	His	Gly	Tyr	Val	Pro	Tyr	Trp	Gly
		115					120					125			
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
	130					135						140			
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	Leu	Thr	Gln	Ser	His
145					150					155					160
Lys	Phe	Leu	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys
				165					170					175	
Ala	Ser	Gln	Asp	Val	Tyr	Asn	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro
			180					185					190		
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Tyr	Thr
		195					200					205			
Gly	Val	Pro	Ser	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Asp	Phe	Thr
	210					215						220			
Phe	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys
225					230					235					240
Gln	Gln	His	Phe	Arg	Thr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	Leu
				245					250					255	
Glu	Ile	Lys	Ala	Leu	Glu	Ile	Ser	Asn	Ser	Val	Met	Tyr	Phe	Ser	Ser
			260					265					270		
Val	Val	Pro	Val	Leu	Gln	Lys	Val	Asn	Ser	Thr	Thr	Thr	Lys	Pro	Val
		275					280					285			
Leu	Arg	Thr	Pro	Ser	Pro	Val	His	Pro	Thr	Gly	Thr	Ser	Gln	Pro	Gln
	290					295					300				
Arg	Pro	Glu	Asp	Cys	Arg	Pro	Arg	Gly	Ser	Val	Lys	Gly	Thr	Gly	Leu
305					310					315					320
Asp	Phe	Leu	Glu	Asp	Pro	Lys	Leu	Cys	Tyr	Leu	Leu	Asp	Gly	Ile	Leu
				325					330					335	

Phe Ile Tyr Gly Val Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe
340 345 350

Ser Arg Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu
355 360 365

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu
370 375 380

Lys Lys Arg Ala Arg Asp Pro Glu Met Gly Gly Lys Gln Gln Arg Arg
385 390 395 400

Arg Asn Pro Gln Glu Gly Val Tyr Asn Ala Leu Gln Lys Asp Lys Met
405 410 415

Ala Glu Ala Tyr Ser Glu Ile Gly Thr Lys Gly Glu Arg Arg Arg Gly
420 425 430

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
435 440 445

Thr Tyr Asp Ala Leu His Met Gln Thr Leu Ala Pro Arg
450 455 460

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr
20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
35 40 45

Gly Trp Ile Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe
50 55 60

Lys Gly Arg Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr
65 70 75 80

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Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys
 85 90 95
 Ala Arg Trp Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe
 130 135 140
 Leu Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser
 145 150 155 160
 Gln Asp Val Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 165 170 175
 Ser Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val
 180 185 190
 Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr
 195 200 205
 Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
 210 215 220
 His Phe Arg Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile
 225 230 235 240
 Lys Ala Leu Glu Ile Ser Asn Ser Val Met Tyr Phe Ser Ser Val Val
 245 250 255
 Pro Val Leu Gln Lys Val Asn Ser Thr Thr Thr Lys Pro Val Leu Arg
 260 265 270
 Thr Pro Ser Pro Val His Pro Thr Gly Thr Ser Gln Pro Gln Arg Pro
 275 280 285
 Glu Asp Cys Arg Pro Arg Gly Ser Val Lys Gly Thr Gly Leu Asp Phe
 290 295 300
 Leu Glu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile
 305 310 315 320
 Tyr Gly Val Ile Ile Thr Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg
 325 330 335
 Ser Ala Glu Thr Ala Ala Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn
 340 345 350
 Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys
 355 360 365

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Arg	Ala	Arg	Asp	Pro	Glu	Met	Gly	Gly	Lys	Gln	Gln	Arg	Arg	Arg	Asn
370						375					380				
Pro	Gln	Glu	Gly	Val	Tyr	Asn	Ala	Leu	Gln	Lys	Asp	Lys	Met	Ala	Glu
385					390					395					400
Ala	Tyr	Ser	Glu	Ile	Gly	Thr	Lys	Gly	Glu	Arg	Arg	Arg	Gly	Lys	Gly
				405					410					415	
His	Asp	Gly	Leu	Tyr	Gln	Gly	Leu	Ser	Thr	Ala	Thr	Lys	Asp	Thr	Tyr
			420					425					430		
Asp	Ala	Leu	His	Met	Gln	Thr	Leu	Ala	Pro	Arg					
		435					440								

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTGAAAGCTT AGATCTGCCC GTGAGGGAGA AATGCCCTGG C

41

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TCGATCTAGA AAGTCCAATC CGGTCCCCTT CACTG

35

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

006T90"4429660

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GATCTCTAGA GGATCCCAAA CTCTGCTACT TGC

33

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGATCTAGA GATCAGCAAC TCGGTGATGT ACTTCAG

37

006790-429560